

IN THE SPECIFICATION:

On Page 3, please delete the third full paragraph and insert the following new paragraph:

It has been determined that some viral leaders have sequence elements involved in translation enhancer activities, such as the CCTTTAGGTT (SEQ. ID. NO. 23) sequence conserved in carlavirus leaders like Potato Virus S (PVS) (Turner R; Bate N; Tewell D; Foster G.D. Arch. Virol. 1994, **134**:321-333) and the so-called internal control regions type 2 (ICR2) motif (GGTTCGANTCC) (SEQ. ID. NO. 24), which is found in 27-base repeated regions in the RNA3 leader of Alfalfa Mosaic Virus (AIMV), needing two to reach optimal translation levels (van der Vossen E.A.G; Neeleman L; Bol J.F. Nucleic Acids Res. 1993, **21**:1361-1367).

On Page 10, after the heading “ Description of the Drawings” please delete the first paragraph and insert the following new paragraph:

Figure 1. Rice Actin-1 (Act) (SEQ. ID. NO. 25), maize ubiquitin-1 (Ubi) (SEQ. ID. NO. 26) and maize sucrose synthase (Shrun) (SEQ. ID. NO. 27) gene sequences from the transcription initiation site. In uppercase is shown the first exon and in lowercase the first intron 5' region and the localization of the repeated and common sequence motifs are underlined.

On Page 10, after the heading “ Description of the Drawings” please delete the second paragraph and insert the following new paragraph:

Figure 2. Eureka artificial translational enhancer sequence, where its relevant elements and restriction endonucleases recognition sites are shown (5' → 3' SEQ. ID. NO. 28), (3' → 5' SEQ. ID. NO. 29).

On Page 10, after the heading “ Description of the Drawings” please delete the third paragraph and insert the following new paragraph:

Figure 3. ART Exon/Intron/Exon artificial sequence (SEQ. ID. NO. 30), showing the origin of each of its component fragments (lowercase: artificial intron; the bases inserted to create UUUUUAU-like sequences are double-underlined; simply underlined are marked some relevant recognition sites for restriction endonucleases).

On Page 11, please delete the first paragraph and insert the following new paragraph:

Figure 4. Primary structure of this invention object (PARTE promoter) (SEQ. ID. NO. 31), showing the core promoter (lowercase italic) fused to the ART Exon/Intron/Exon region (intron bases in lowercase, exon's in uppercase) and to the artificial translational enhancer EUREKA. Some relevant recognition sites for restriction endonucleases are underlined; TATA box is double-underlined and translation initiation codon is in bold.

On Page 11, please delete the second paragraph and insert the following new paragraph:

Figure 5. Primary structure of the APARTE promoter (SEQ. ID. NO. 32), showing rice actin-1 5' regulatory region (region from -43 to -310 from the transcription initiation site, in italics uppercase) fused to PARTE promoter (in italics lowercase the promoter, in lowercase the intron; in uppercase the exons). Underlined are marked some relevant recognition sites for restriction endonucleases; TATA box is double-underlined and the translation initiation codon is in bold.

On Page 11, please delete the third paragraph and insert the following new paragraph:

Figure 6. Primary structure of the U3ARTE promoter (SEQ. ID. NO. 33), showing its component elements: -299 to -855 region from the maize *ubi-1* gene transcription initiation site, in uppercase; *as-1*-like transcription enhancer, in bold uppercase; region from -43 to -310 from the transcription initiation site of the rice *act-1* gene, in italics uppercase; PARTE promoter in lowercase (TATA box is double underlined, ART intron is in italics and the translation initiation site is simple underlined).

On Page 11, please delete the fifth paragraph and insert the following new paragraph:

Figure 8. Primary structure of GARTE promoter (SEQ. ID. NO. 34), showing its component elements: rice *gluB-1* gene region from -31 to -245 from the transcription initiation site, in italics uppercase; PARTE promoter (promoter is in italics lowercase, intron in lowercase; exons are in uppercase; some relevant restriction sites are underlined; TATA-box is double underlined; translation initiation codon is in bold).